

# Genetic Expression Profiles of 18 Genes Regulated by the Filamentation MAPK Pathway

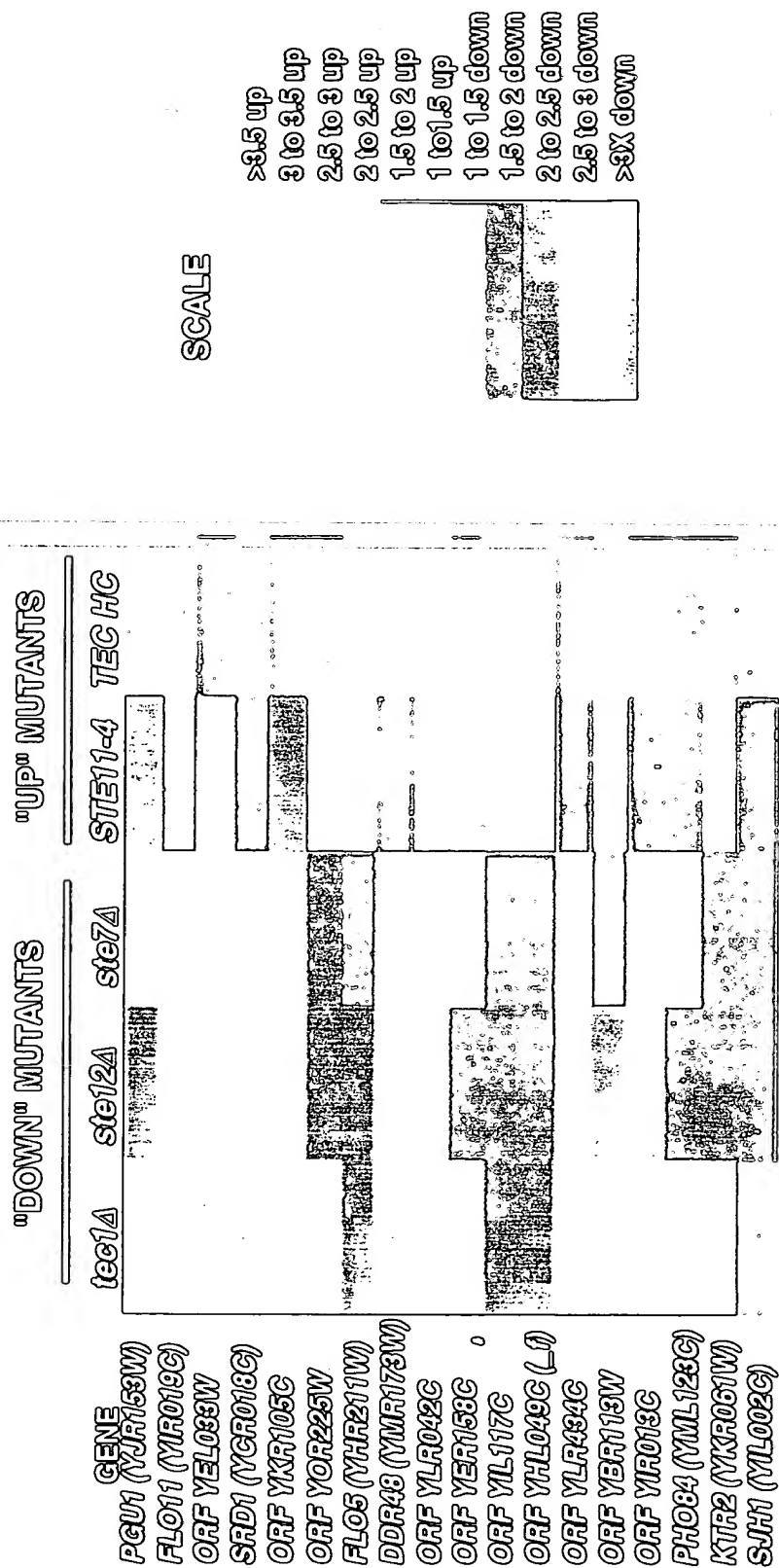


Figure 1

# MAPK Targets Include Proteins Known or Predicted to Enter the Secretory Pathway

<b>PGU1</b>	secreted endopolygalacturonase
<b>FLO11</b>	GPI-linked cell surface adhesion factor
<b>TOT10/YEL033W</b>	novel
<b>SRD1</b>	Zinc finger protein
<b>TOT12/YKR105C</b>	putative permease
<b>TOT13/YOR225W</b>	putative membrane protein
<b>FLO5</b>	GPI-linked cell surface adhesion factor
<b>DDR48</b>	cell surface protein
<b>TOT11/YLR042C</b>	GPI-linked cell surface protein
<b>TOT7/YER158C</b>	Homolog of mating morphogenesis protein Afr1
<b>TOT8/YIL117C</b>	Homolog of Chitin Synthase III subunit
<b>TOT20/YHL049C</b>	telomeric protein family member
<b>TOT15/YLR434C</b>	novel
<b>TOT14/YBR113W</b>	putative membrane protein
<b>TOT9/YIR013C</b>	Zinc finger protein
<b>PHO84</b>	phosphate transporter, sugar permease family
<b>KTR2</b>	protein mannosyltransferase homolog
<b>SJH1</b>	Sac1-related inositol phosphate 5-phosphatase homolog

Figure 2

# Sytematic Knockout Experiments

GENE	Haploid Invasion	Diploid Filamentation
<i>PGU1</i>	+++	+++
<i>FLO11</i>	-	-
<i>TOT10/YEL033W</i>	+	+
<i>SRD1</i>	ND	ND
<i>TOT12/YKR105C</i>	+++	+++
<i>TOT13/YOR225W</i>	+++	+++
<i>FLO5</i>	+++	+++
<i>DDR48</i>	+++	+++
<i>TOT11/YLR042C</i>	+++	+++
<i>TOT7/YER158C</i>	+++	+++
<i>TOT8/YIL117C</i>	+++	+++
<i>TOT20/YHL049C</i>	ND	ND
<i>TOT15YLR434C</i>	+++	+++
<i>TOT14/YBR113W</i>	+++	+++
<i>TOT9/YIR013C</i>	+++	+++
<i>PHO84</i>	+++	+++
<i>KTR2</i>	+++	+++
<i>SJH1</i>	+++	+++

Figure 3

# Filamentation MAPK Pathway Controls Pectinolysis via PGU1

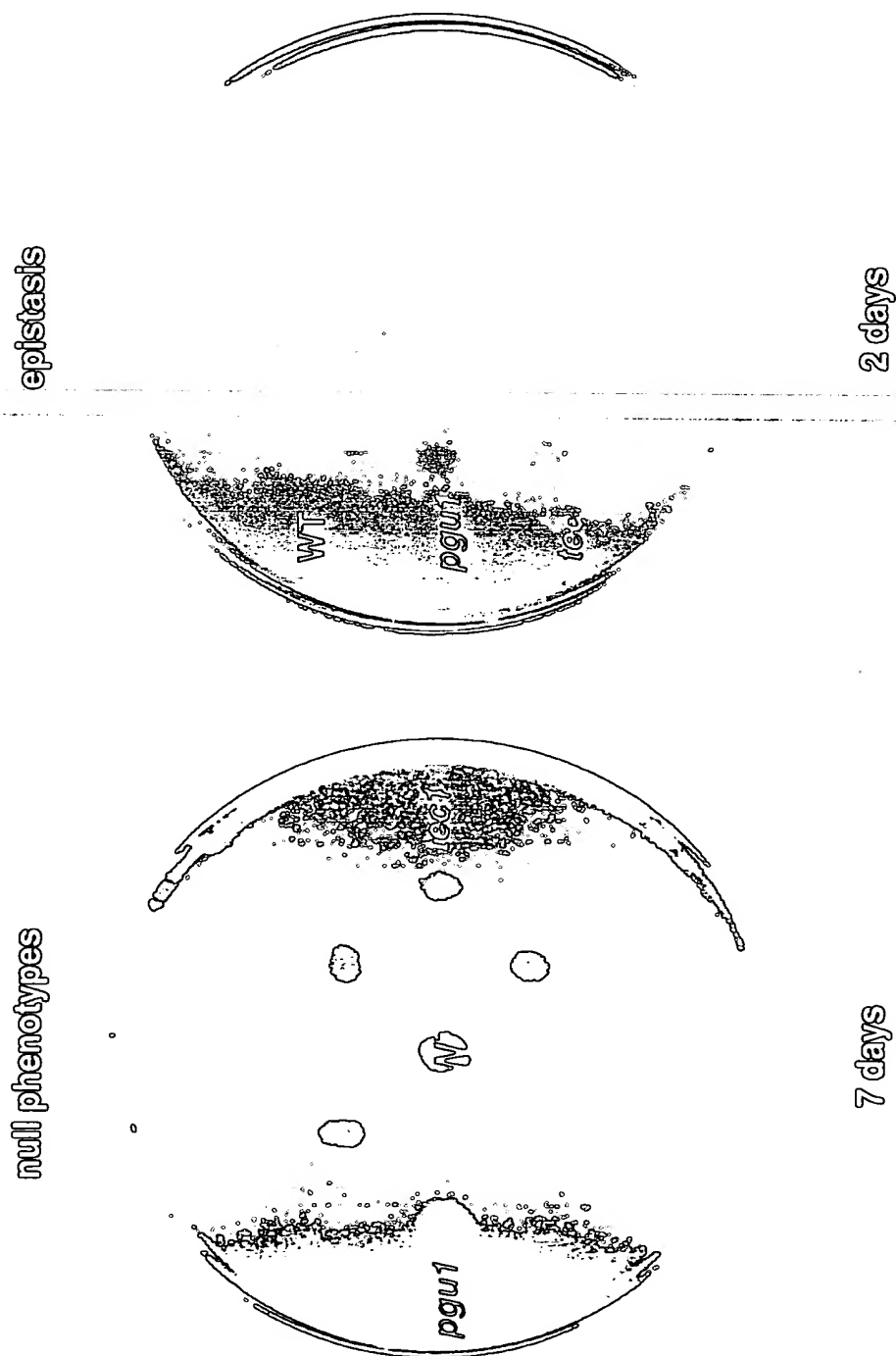


Figure 4

# Gene Induction by the Plant-Specific Carbohydrate Polygalacturonic Acid and Its Hydrolysis Product

## Genes Selectively Induced by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>XBP1</i>	2.40	6.65	Stress-induced transcriptional repressor
<i>YHR217C</i> (f)	1.30	6.00	Protein of unknown function
<i>YPL080C</i>	2.80	5.70	Protein of unknown function
<i>YPR098C</i>	1.16	5.49	Protein of unknown function
<i>YHL040C</i>	2.04	5.00	Putative MFS Permease
<i>YOL080C</i>	1.35	4.74	Protein with similarity to Rnh70p and Pan2p
<i>PHO84</i>	1.39	4.70	phosphate transport, sugar permease homolog*
<i>YMR293C</i>	1.29	4.07	Protein with similarity to amidase
<i>YLR184W</i>	1.33	3.24	Protein of unknown function
<i>YIL011W</i>	1.01	3.01	Protein with similarity to PAU1 family
<i>CYT1</i>	1.02	2.82	Cytochrome c1
<i>ATP11</i>	1.29	2.65	F1-ATP synthase assembly protein
<i>YOR091W</i>	1.17	2.51	Protein of unknown function
<i>PAU3</i>	1.02	2.46	Stress-induced protein of the PAU1 family
<i>SKO1</i>	0.47	2.35	ATF/CREB transcriptional repressor
<i>MSI4</i>	0.73	2.06	Rab guanine nucleotide dissociation inhibitor
Regulated by Filamentation MAPK Pathway*			

## Genes Selectively Induced by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>VPS1</i>	4.03	1.69	Vacuolar sorting protein, dynamin GTPase

Figure 5

# Gene Repression by the Plant-Specific Carbohydrate Polygalacturonic Acid and its Hydrolysis Product

## Genes Selectively Repressed by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
COP1/SEC33	0.63	0.17	alpha subunit of coatamer complex
YOL002C	1.36	0.18	Protein of unknown function
YDL173W	0.96	0.24	Protein of unknown function
COQ2	1.37	0.25	coenzyme Q (ubiquinone) biosynthesis
YIL176C (f)	0.86	0.30	Protein with similarity to PAU1 family
YFL032W	0.80	0.30	Protein of unknown function
RPS33A	1.10	0.34	Ribosomal protein S28A
ARC35	1.25	0.39	Component of ARP2/3 complex
RPS26A	0.87	0.39	Ribosomal protein S26A
RPS10A	1.02	0.46	Ribosomal protein S10A

## Genes Selectively Repressed by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
YEL033W	0.12	0.38	Protein of unknown function*
VID24	0.24	1.46	Vacuolar import and degradation of Fbp1
NDC1	0.29	1.02	Spindle pole body duplication factor
SKO1	0.47	2.35	ATF/CREB transcriptional repressor

\*Regulated by the Filamentation MAPK Pathway

Figure 6

MARK DATA										Note that the details of the list are slightly different from some of the figures because these data were flopped and listed slightly differently.									
file=20	inst=10	scaling=0	WT	lecl	1012	1017	TECHC	STE11-4	YPO Time	data are sorted as TECHC high copy/tech; Tyl elements have been purged									
GENA	282	47	1012	1017	1012	1017	1012	1017	1012										
STAT (TUBOPO)	282	47	1012	1017	1012	1017	1012	1017	1012										
POUT (TUBOPO)	282	47	1012	1017	1012	1017	1012	1017	1012										
ONE TELSON	178	20	34	21	289	20	289	20	289										
ONE TELSON	482	147	107	107	107	107	107	107	107										
ONE TELSON	91	33	20	20	275	20	275	20	275										
ONE TELSON	57	20	20	20	190	20	190	20	190										
ONE TELSON	251	50	44	44	44	44	44	44	44										
ONE TELSON	112	20	44	44	44	44	44	44	44										
ONE TELSON	86	20	47	45	109	45	109	45	109										
ONE TELSON	105	21	51	29	113	29	113	29	113										
ONE TELSON	75	30	48	138	159	159	159	159	159										
ONE TELSON	672	134	384	665	955	955	955	955	955										
ONE TELSON	89	26	20	20	120	20	120	20	120										
ONE TELSON	78	26	20	20	114	20	114	20	114										
ONE TELSON	724	180	348	620	702	702	702	702	702										
ONE TELSON	66	30	66	58	128	58	128	58	128										
ONE TELSON	612	332	45	62	1701	62	1701	62	1701										
ONE TELSON	170	20	20	108	104	104	104	104	104										
ONE TELSON	132	65	119	183	233	233	233	233	233										
ONE TELSON	305	137	187	182	472	182	472	182	472										
ONE TELSON	59	34	57	55	117	55	117	55	117										
ONE TELSON	401	126	327	394	474	394	474	394	474										
ONE TELSON	57	33	75	73	119	73	119	73	119										
ONE TELSON	48	20	105	106	133	106	133	106	133										
ONE TELSON	44	41	102	54	127	54	127	54	127										
ONE TELSON	153	57	133	121	184	121	184	121	184										
ONE TELSON	20	20	20	20	20	20	20	20	20										
ONE TELSON	54	31	146	70	257	70	257	70	257										
ONE TELSON	1042	655	697	731	1731	731	1731	731	1731										
ONE TELSON	153	45	54	40	115	40	115	40	115										
ONE TELSON	104	39	137	133	189	133	189	133	189										
ONE TELSON	102	61	118	99	149	99	149	99	149										
ONE TELSON	149	76	176	186	161	186	161	186	161										
ONE TELSON	82	38	90	121	192	121	192	121	192										
ONE TELSON	86	66	36	59	202	59	202	59	202										
ONE TELSON	204	42	76	120	177	120	177	120	177										
ONE TELSON	47	47	20	105	20	105	20	105	20										
ONE TELSON	255	106	176	125	236	125	236	125	236										
ONE TELSON	232	178	159	182	3493	182	3493	182	3493										
ONE TELSON	53	39	59	59	84	59	84	59	84										
ONE TELSON	779	460	1410	1405	971	1405	971	1405	971										
ONE TELSON	887	842	717	632	1775	632	1775	632	1775										
ONE TELSON	239	200	459	230	415	230	415	230	415										
ONE TELSON	1947	1008	2058	1789	2089	1789	2089	1789	2089										
ONE TELSON	1555	820	1815	1324	1697	1324	1697	1324	1697										
ONE TELSON	48	66	58	47	135	47	135	47	135										
ONE TELSON	105	63	119	85	127	85	127	85	127										
ONE TELSON	650	428	327	274	658	274	658	274	658										
ONE TELSON	765	607	676	495	1216	495	1216	495	1216										
ONE TELSON	168	174	253	149	348	149	348	149	348										
ONE TELSON	60	20	114	91	440	91	440	91	440										
ONE TELSON	127	63	85	115	126	115	126	115	126										
ONE TELSON	87	38	77	122	78	122	78	122	78										
ONE TELSON	73	43	109	43	199	43	199	43	199										
ONE TELSON	41	41	121	121	121	121	121	121	121										

Figure 7

NAME=GA						
gene	YPD	GA	PGA	GA/YPD	PGA/YPD	
ORF YIL101C	20	48	133	2.40	6.65	
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.30	
ORF YHR217C (_r_i)	20	29	120	1.45	6.00	
ORF YHR217C (_f)	20	26	120	1.30	6.00	
ORF YPL080C	20	56	114	2.80	5.70	
ORF YPR098C	37	43	203	1.16	5.49	
ORF YHL040C	27	55	135	2.04	5.00	
ORF YOL080C	23	31	109	1.35	4.74	
PHO84 (YML123C)	33	46	155	1.39	4.70	
ORF YMR293C	28	36	114	1.29	4.07	
ORF YLR184W	66	88	214	1.33	3.24	
ORF YIL011W	153	154	460	1.01	3.01	
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94	
CYT1 (YOR065W)	91	93	257	1.02	2.82	
ORF YLL025W (_f)	251	355	693	1.41	2.76	
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73	
ATP11 (YNL315C)	51	66	135	1.29	2.65	
ORF YOR091W	59	69	148	1.17	2.51	
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.50	
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46	
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46	
SKO1 (YNL167C)	43	20	101	0.47	2.35	
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15	
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12	
ORF YNL006W	77	100	161	1.30	2.09	
MSI4 (YOR370C)	63	46	130	0.73	2.06	
ORF YPR139C	91	122	187	1.34	2.05	
SPO15 (YKR001C)	35	141	59	4.03	1.69	
HHO1 (YPL127C)	81	45	135	0.56	1.67	
ILV3 (YJR016C)	119	72	182	0.61	1.53	
ORF YBR105C	82	20	120	0.24	1.46	
LYS4 (YDR234W)	479	244	576	0.51	1.20	
ORF YOR009W	144	310	158	2.15	1.10	
NDC1 (YML031W)	113	33	115	0.29	1.02	
ORF YOL073C	143	180	88	1.26	0.62	
ORF YJL223C (_f)	134	175	81	1.31	0.60	
ORF YMR242C	1170	1227	610	1.05	0.52	
ORF YOR248W (_f)	497	422	239	0.85	0.48	
ORF YPL081W exon 1	159	135	75	0.85	0.47	
ORF YML019W	177	91	82	0.51	0.46	
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46	
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45	
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39	
ORF YNR035C	200	249	78	1.25	0.39	
ORF YEL033W	172	20	66	0.12	0.38	
TSL1 (YML100W)	103	20	39	0.19	0.38	
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34	
ORF YFL032W	122	98	37	0.80	0.30	
ORF YIL176C (_f)	115	99	34	0.86	0.30	
COQ2 (YNR041C)	84	115	21	1.37	0.25	
ORF YDL173W	141	136	34	0.96	0.24	
ORF YOL002C	111	151	20	1.36	0.18	
ORF YDL145C	118	74	20	0.63	0.17	
PROCESS=scaling	METHOD=bulk SOURCE=GA.scd					
PROCESS=assemble.pl	GENES=6365 SOURCE=					
PROCESS=filter	GENES=53 DIFF=80 MAX= RAT=2					
=						

Figure 8



NAME=GA						
gene	YPD	GA	PGA	GA/YPD	PGA/YPD	
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.30	
SPO15 (YKR001C)	35	141	59	4.03	1.69	
ORF YPL080C	20	56	114	2.80	5.70	
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73	
ORF YIL101C	20	48	133	2.40	6.65	
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.50	
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94	
ORF YOR009W	144	310	158	2.15	1.10	
ORF YHL040C	27	55	135	2.04	5.00	
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15	
ORF YHR217C (_r_i)	20	29	120	1.45	6.00	
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12	
ORF YLL025W (_f)	251	355	693	1.41	2.76	
PHO84 (YML123C)	33	46	155	1.39	4.70	
COQ2 (YNR041C)	84	115	21	1.37	0.25	
ORF YOL002C	111	151	20	1.36	0.18	
ORF YOL080C	23	31	109	1.35	4.74	
ORF YPR139C	91	122	187	1.34	2.05	
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46	
ORF YLR184W	66	88	214	1.33	3.24	
ORF YJL223C (_f)	134	175	81	1.31	0.60	
ORF YHR217C (_f)	20	26	120	1.30	6.00	
ORF YNL006W	77	100	161	1.30	2.09	
ATP11 (YNL315C)	51	66	135	1.29	2.65	
ORF YMR293C	28	36	114	1.29	4.07	
ORF YOL073C	143	180	88	1.26	0.62	
ORF YNR035C	200	249	78	1.25	0.39	
ORF YOR091W	59	69	148	1.17	2.51	
ORF YPR098C	37	43	203	1.16	5.49	
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34	
ORF YMR242C	1170	1227	610	1.05	0.52	
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46	
CYT1 (YOR065W)	91	93	257	1.02	2.82	
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46	
ORF YIL011W	153	154	460	1.01	3.01	
ORF YDL173W	141	136	34	0.96	0.24	
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39	
ORF YIL176C (_f)	115	99	34	0.86	0.30	
ORF YOR248W (_f)	497	422	239	0.85	0.48	
ORF YPL081W exon 1	159	135	75	0.85	0.47	
ORF YFL032W	122	98	37	0.80	0.30	
MSI4 (YOR370C)	63	46	130	0.73	2.06	
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45	
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ORF YEL033W	172	20	66	0.12	0.38	
PROCESS=scaling	METHOD=bulk SOURCE=GA.scf					
PROCESS=assemble.pl	GENES=6365 SOURCE=					
PROCESS=filter	GENES=53 DIFF=80 MAX= RAT=2					
=						

Figure 9

# Homologous Genes Induced by Filamentation and Mating MAPK Pathways

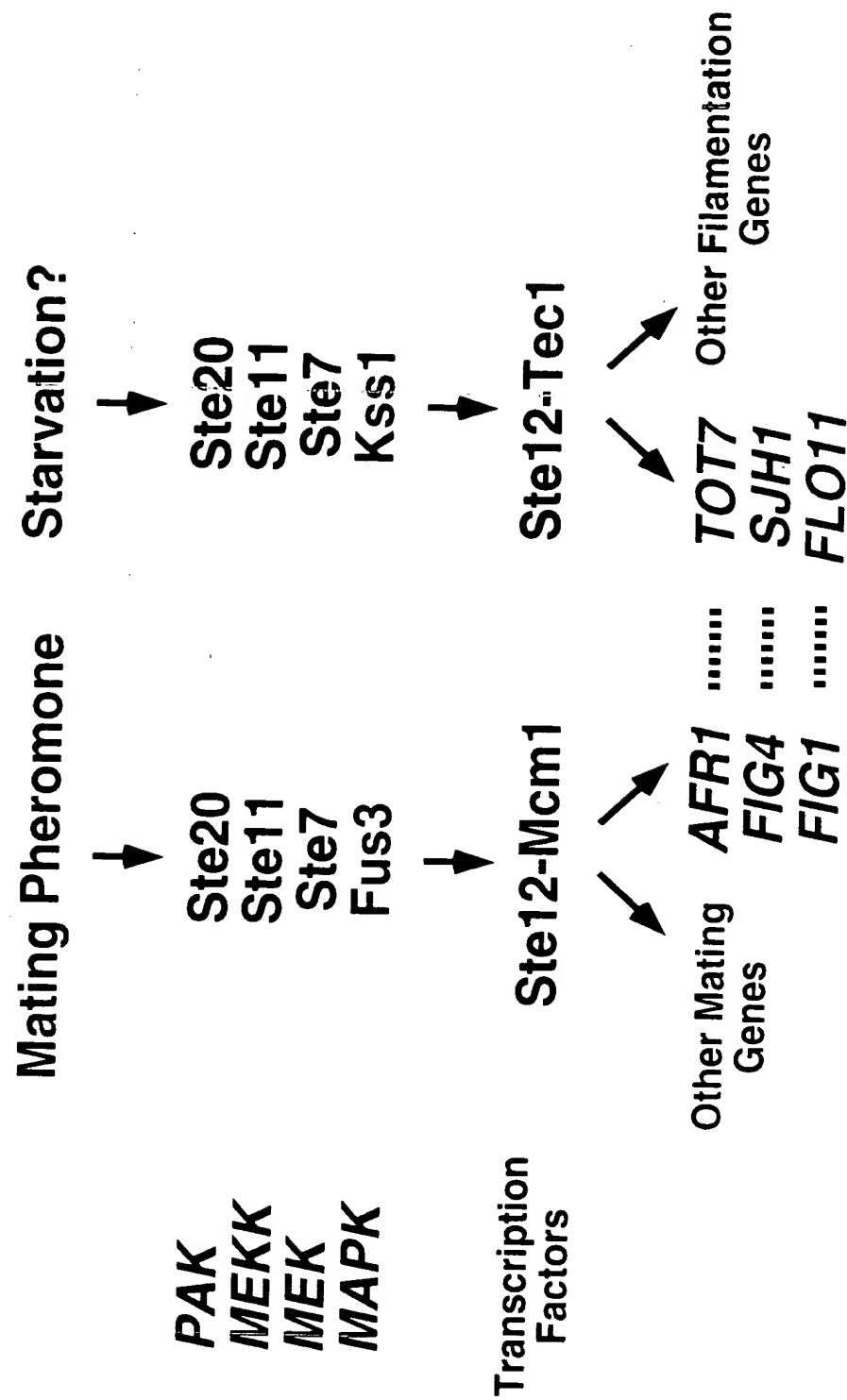


Figure 10

